



#6

-54-

SEQUENCE LISTING

(1)

GENERAL INFORMATION:

- (i) APPLICANT: HUMAN GENOME SCIENCES, INC.  
9410 KEY WEST AVENUE  
ROCKVILLE, MD 20850  
UNITED STATES OF AMERICA

APPLICANTS/INVENTORS: LI, YI  
CAO, LIANG  
ROSEN, CRAIG A.

(ii) TITLE OF INVENTION: Human G-Protein Coupled Receptor

(iii) NUMBER OF SEQUENCES: 30

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
- (B) STREET: 1100 NEW YORK AVE., NW, SUITE 600
- (C) CITY: WASHINGTON
- (D) STATE: DC
- (E) COUNTRY: USA
- (F) ZIP: 20005

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: FLOPPY DISK
- (B) COMPUTER: IBM PC COMPATIBLE
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US95/04079
- (B) FILING DATE: 30-MAR-1995
- (C) CLASSIFICATION:

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/765,973
- (B) FILING DATE: 06-JUN-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: STEFFE, ERIC K.
- (B) REGISTRATION NUMBER: 36,688
- (C) REFERENCE/DOCKET NUMBER: 1488.114PC00/EKS/KLM

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-371-2600
- (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 116..1003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGT CATTCAACAT TTATTCAACC AAAAATACTA AGTCAGCTCT ATACAAACTA	60
ATGGAAGGAT ACAGCTATGC AAATATAGAA CACTAAAGTG TTACATGACA GATGT ATG	118
Met	
1	
AGT AGT GAA ATG GTG AAA AAT CAG ACA ATG GTC ACA GAG TTC CTC CTA	166
Ser Ser Glu Met Val Lys Asn Gln Thr Met Val Thr Glu Phe Leu Leu	
5 10 15	
CTG GGA TTT CTC CTG GGC CCA AGG ATT CAG ATG CTC CTC TTT GGG CTC	214
Leu Gly Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu	
20 25 30	
TTC TCC CTG TTC TAT GTC TTC ACC CTG CTG GGG AAT GGG ACC ATC CTG	262
Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu	
35 40 45	
GGG CTC ATC TCA CTG GAC TCC AGA CTC CAC ACC CCC ATG TAC TTC TTC	310
Gly Leu Ile Ser Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe	
50 55 60 65	
CTC TCA CAC CTG GCC GTC GTC AAC ATC GCC TAT GCC TGC AAC ACA GTG	358
Leu Ser His Leu Ala Val Val Asn Ile Ala Tyr Ala Cys Asn Thr Val	
70 75 80	
CCC CAG ATG CTG GTG AAC CTC CTG CAT CCA GCC AAG CCC ATC TCC TTT	406
Pro Gln Met Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe	
85 90 95	
GCT GGT TGC ATG ACA CTA GAC TTT CTC TTT TTG AGT TTT GCA CAT ACT	454
Ala Gly Cys Met Thr Leu Asp Phe Leu Phe Leu Ser Phe Ala His Thr	
100 105 110	
GAA TGC CTC CTG TTG GTG CTG ATG TCC TAC GAT CGG TAC GTG GCC ATC	502
Glu Cys Leu Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Ile	
115 120 125	
TGC CAC CCT CTC CGA TAT TTC ATC ATC ATG ACC TGG AAA GTC TGC ATC	550
Cys His Pro Leu Arg Tyr Phe Ile Ile Met Thr Trp Lys Val Cys Ile	
130 135 140 145	
ACT CTG GGC ATC ACT TCC TGG ACA TGT GGC TCC CTC CTG GCT ATG GTC	598
Thr Leu Gly Ile Thr Ser Trp Thr Cys Gly Ser Leu Leu Ala Met Val	
150 155 160	
CAT GTG AGC CTC ATC CTA AGA CTG CCC TTT TGT GGG CCT CGT GAA ATC	646
His Val Ser Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Arg Glu Ile	
165 170 175	
AAC CAC TTC TTC TGT GAA ATC CTG TCT GTC CTC AGG CTG GCC TGT GCT	694
Asn His Phe Phe Cys Glu Ile Leu Ser Val Leu Arg Leu Ala Cys Ala	
180 185 190	
GAT ACC TGG CTC AAC CAG GTG GTC ATC TTT GAA GCC TGC ATG TTC ATC	742

Asp Thr Trp Leu Asn Gln Val Val Ile Phe Glu Ala Cys Met Phe Ile	
195 200 205	
CTG GTG GGA CCA CTC TGC CTG GTG CTG GTC TCC TAC TCA CAC ATC CTG	790
Leu Val Gly Pro Leu Cys Leu Val Leu Val Ser Tyr Ser His Ile Leu	
210 215 220 225	
GGG GGC ATC CTG AGG ATC CAG TCT GGG GAG GGC CGC AGA AAG GCC TTC	838
Gly Gly Ile Leu Arg Ile Gln Ser Gly Glu Gly Arg Arg Lys Ala Phe	
230 235 240	
TCC ACC TGC TCC TCC CAC CTC TGC GTA GTG GGA CTC TTC TTT GGS AGC	886
Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Phe Gly Ser	
245 250 255	
GCC ATC GTC ATG TAC ATG GCC CCT AAG TCC CGC CAT CCT GAG GAG CAG	934
Ala Ile Val Met Tyr Met Ala Pro Lys Ser Arg His Pro Glu Glu Gln	
260 265 270	
CAG AAG GTC CTT TTT CTT ATT TTA CAG TTC CTT TCA ACC CCG ATG CTT	982
Gln Lys Val Leu Phe Leu Ile Leu Gln Phe Leu Ser Thr Pro Met Leu	
275 280 285	
AAA CCC CCT GAT TTA CAA CCC TGA GGAATGTAGA GGGTCAAGGG TGCCCTCCGA	1036
Lys Pro Pro Asp Leu Gln Pro	
290 295	
GGAGACCACT GTGCAARGRA AGTCATTCCT AAGGGGTGTG ACATTTGAAC TGCCAGCCCC	1096
AGTTGCCCCG TGGACTCCTG ATGCCCAATT ATTGCCTCAA CCCAGAAAAG TTTACTCCCC	1156
TTTAACTGTG CTTTACTGAC AGAAGGGCAA GCCTTCTCCC GTTTTTTGCA GATAAAATTT	1216
TAGATGTGTT GCAATCATTG GGTTTCTAGG AGATGTGGTT TTATCAGACA ATTTTTTCTT	1276
TTATTTTACA ATTACTTTAA TATCTGTAAA ATAAAGAATT ATTTTAAATC ATTTTCCAG	1336
TCCCAAAAGT TAAATACAGG CCACTTACTT CTTTAACCAA ATGATATAGT TTGGCTCTGT	1396
GTCCCCACCC AAATCTCATG TCAAATTGTA ATCCCCGCAT GTCAGCGGAG GGACCTGGTG	1456
GGAGGTGATT GGATCATGGG GAGGGATTTC CCCCTTGCTG TTCTGTTGAT AGTGAACGAG	1516
TTCTCACGAA ATCTGATGGT TTAAAAGTGC AGCACTTCTC CCTTTGCTCT CTCTCTCCTG	1576
CTGTGCCATG GTAAGACGTG CCTTGCTTCC CCTGGTGCTT CCGCCATGAT TGTACCTTTC	1636
CTGAGGCCTC TCCAGCCATG TGGAAGTGTG AGCCAATTAA ACTTCTTTTC TTTAGAAAAA	1696
AAAAAAAAA AAAAAAA	1713

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Glu	Met	Val	Lys	Asn	Gln	Thr	Met	Val	Thr	Glu	Phe	Leu	1	5	10	15
Leu	Leu	Gly	Phe	Leu	Leu	Gly	Pro	Arg	Ile	Gln	Met	Leu	Leu	Phe	Gly	20	25	30	
Leu	Phe	Ser	Leu	Phe	Tyr	Val	Phe	Thr	Leu	Leu	Gly	Asn	Gly	Thr	Ile	35	40	45	
Leu	Gly	Leu	Ile	Ser	Leu	Asp	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	50	55	60	
Phe	Leu	Ser	His	Leu	Ala	Val	Val	Asn	Ile	Ala	Tyr	Ala	Cys	Asn	Thr	65	70	75	80
Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Leu	His	Pro	Ala	Lys	Pro	Ile	Ser	85	90	95	
Phe	Ala	Gly	Cys	Met	Thr	Leu	Asp	Phe	Leu	Phe	Leu	Ser	Phe	Ala	His	100	105	110	
Thr	Glu	Cys	Leu	Leu	Leu	Val	Leu	Met	Ser	Tyr	Asp	Arg	Tyr	Val	Ala	115	120	125	
Ile	Cys	His	Pro	Leu	Arg	Tyr	Phe	Ile	Ile	Met	Thr	Trp	Lys	Val	Cys	130	135	140	
Ile	Thr	Leu	Gly	Ile	Thr	Ser	Trp	Thr	Cys	Gly	Ser	Leu	Leu	Ala	Met	145	150	155	160
Val	His	Val	Ser	Leu	Ile	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Pro	Arg	Glu	165	170	175	
Ile	Asn	His	Phe	Phe	Cys	Glu	Ile	Leu	Ser	Val	Leu	Arg	Leu	Ala	Cys	180	185	190	
Ala	Asp	Thr	Trp	Leu	Asn	Gln	Val	Val	Ile	Phe	Glu	Ala	Cys	Met	Phe	195	200	205	
Ile	Leu	Val	Gly	Pro	Leu	Cys	Leu	Val	Leu	Val	Ser	Tyr	Ser	His	Ile	210	215	220	
Leu	Gly	Gly	Ile	Leu	Arg	Ile	Gln	Ser	Gly	Glu	Gly	Arg	Arg	Lys	Ala	225	230	235	240
Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Phe	Gly	245	250	255	
Ser	Ala	Ile	Val	Met	Tyr	Met	Ala	Pro	Lys	Ser	Arg	His	Pro	Glu	Glu	260	265	270	
Gln	Gln	Lys	Val	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Leu	Ser	Thr	Pro	Met	275	280	285	
Leu	Lys	Pro	Pro	Asp	Leu	Gln	Pro	290	295										

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2185 base pairs

(B) TYPE: nucleic acid

(ix) FEATURE:

(B) LOCATION: 884..2062

TC	ACT	TAT	AGG	GCG	AAT	TGGG	TAC	GGG	CCCC	CC	CT	CG	AGGT	CG	AC	GGT	TATC	GAT	AAG	CTTG	60	
AT	AT	CGA	AAT	CGG	CAC	GAG	CG	GGG	CT	CGG	A	GAG	GT	GAC	CGG	GGG	CT	GG	TAG	CAT	AG	120
TT	TG	AAT	TTGA	TG	AT	TGG	AGC	CC	AAC	CAC	AGG	GGG	TT	TGG	AG	CT	TGG	TAC	CGG	TGAA	GCT	180
AAA	AGG	TT	TCC	TGG	AG	TAG	AC	GAT	TGG	AG	CCA	TA	ACT	TGG	AAC	CGG	AG	TCT	TGT	GA	ATGA	240
AGG	AC	AGG	AG	CAG	CAC	CT	TGG	CG	AT	TGG	TGCC	AGG	ACC	CGG	AA	GAG	GAG	CC	CAG	AGG	AGG	300
GG	AGA	AGG	AG	CC	AGA	ATT	TGC	TGT	CT	TGT	TGGA	GCC	GCC	CAT	AG	GAG	CC	AG	AGG	GGT	TG	360
GC	CT	GAGA	AAT	GC	AGA	AAG	ATG	CT	TGG	AG	CC	CAG	CC	CAG	AA	GAG	CT	TGG	AG	CT	TG	420
TG	CT	GAC	CGGA	AA	AGG	ACT	TGG	CC	CAG	AG	CCGA	AG	CT	TGG	CACC	AGG	GAC	AGG	G	AGG	T	480
GGG	CC	ACG	GT	TG	AG	TT	CAAC	CC	ACT	G	ACTT	CAG	G	TGA	AAG	ACT	TG	TG	ACC	AG	CTT	540
GAG	GC	CCT	CAC	CAG	AG	TGG	GT	GGG	GG	CAT	G	GGG	G	CT	CG	CAG	TAC	CC	CAG	AG	TAG	600
GG	TAG	CCCC	GG	CC	AGG	GG	TTA	ACG	TGG	GG	GCG	TG	GAT	T	CAAC	AC	AG	CTT	TGGA	AG	CCC	660
TCG	GAG	GGCC	CCC	GGG	TG	CTT	TGG	GCC	AAT	TG	AG	GA	CAG	GAG	T	CAG	TCC	CAT	CC	CG	AGG	720
GT	CT	CACT	AC	AAT	CTT	CACA	CG	CCT	TT	TATT	ATT	CAC	CAT	G	TTG	GGT	TG	GC	CA	CCT	TG	780
AG	CA	AG	CGGA	AGG	CT	GAGG	C	CAG	TAG	GGG	G	AGG	GGT	TG	TTA	CT	GGG	GGT	TCG	AAG	AAG	840
CAC	AG	AG	ACA	GGG	G	TAGG	G	CAG	GGG	G	TCGG	GG	CC	CAC	GG	CC	TGG	ATG	AGG	CCC	ACA	895
																		Met	Arg	Pro	Thr	
																		1				
TGG	GCA	GGC	TGG	CTG	ATG	AGA	TGG	TGC	TGC	CCC	CCT	GCT	GAC	ACG	AGG							943
Trp	Ala	Gly	Trp	Leu	Met	Arg	Trp	Cys	Cys	Pro	Pro	Ala	Asp	Thr	Arg							
5					10					15					20							
TGC	ACC	ACA	TTC	CTT	TGC	AGC	GGG	CGG	GCT	GCC	CCA	CAG	CAA	GCT	GGC							991
Cys	Thr	Thr	Phe	Leu	Cys	Ser	Gly	Arg	Ala	Ala	Pro	Gln	Gln	Ala	Gly							
				25					30					35								
GCA	CCT	GGG	CAC	CAT	CCA	AAA	TAC	AGC	TTG	TTT	CCC	TGG	ATT	TGG	AAG							1039
Ala	Pro	Gly	His	His	Pro	Lys	Tyr	Ser	Leu	Phe	Pro	Trp	Ile	Trp	Lys							
				40				45					50									
GTG	AGA	GGT	TTG	CTT	CCC	CCT	CCA	TTA	ACC	ACT	GAC	GTT	GTG	CCA	GTG							1087
Val	Arg	Gly	Leu	Leu	Pro	Pro	Pro	Leu	Thr	Thr	Asp	Val	Val	Pro	Val							
				55				60					65									
AGA	CTA	ACT	CTC	CGC	GCC	AAT	CTG	TCC	GCG	GCT	GAC	CTC	CTT	CGC	GGG							1135

Arg	Leu	Thr	Leu	Arg	Ala	Asn	Leu	Ser	Ala	Ala	Asp	Leu	Leu	Arg	Gly	
70						75					80					
CGT	GGC	CTA	CCT	CTT	CCT	CAT	GTT	CCA	CAC	TGT	CCC	CGC	ACA	GCC	CGA	1183
Arg	Gly	Leu	Pro	Leu	Pro	His	Val	Pro	His	Cys	Pro	Arg	Thr	Ala	Arg	
85					90					95					100	
CTT	TCA	CTT	GAG	GGC	TGG	TTC	CTG	CGG	CAG	GGC	TTG	CTG	GAC	ACA	AAC	1231
Leu	Ser	Leu	Glu	Gly	Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Thr	Asn	
				105					110					115		
CTC	ACT	GCG	TCG	GTG	GCC	ACA	CTG	CTG	GCC	ATC	GCC	GTG	GAG	CGG	CAC	1279
Leu	Thr	Ala	Ser	Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala	Val	Glu	Arg	His	
			120						125				130			
CGC	AGT	GTG	ATG	GCC	GTG	CAG	CTG	CAC	AGC	CGC	CTG	CCC	CGT	GGC	CGC	1327
Arg	Ser	Val	Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu	Pro	Arg	Gly	Arg	
		135					140					145				
GTG	GTC	ATG	CTC	ATT	GTG	GGC	GTG	TGG	GTG	GCT	GCC	CTG	GGC	CTG	GGG	1375
Val	Val	Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	Leu	Gly	Leu	Gly	
	150					155					160					
CTG	CTG	CCT	GCC	CAC	TCC	TGG	CAC	TGC	CTC	TGT	GCC	CTG	GAC	CGC	TCC	1423
Leu	Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala	Leu	Asp	Arg	Ser	
165					170					175					180	
TCA	CGC	ATG	GCA	CCC	CTG	CTC	AGC	CGC	TCC	TAT	TTG	GCC	GTC	TGG	GCT	1471
Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu	Ala	Val	Trp	Ala	
				185					190					195		
CTG	TCG	AGC	CTG	CTT	GTC	TTC	CTG	CTC	ATG	GTG	GCT	GTG	TAC	ACC	CGC	1519
Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala	Val	Tyr	Thr	Arg	
			200						205				210			
ATT	TTC	TTC	TAC	GTG	CGG	CGG	CGA	GTG	CAG	CGC	ATG	GCA	GAG	CAT	GTC	1567
Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met	Ala	Glu	His	Val	
		215					220					225				
AGC	TGC	CAC	CCC	CGC	TAC	CGA	GAG	ACC	ACG	CTC	AGC	CTG	GTC	AAG	ACT	1615
Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser	Leu	Val	Lys	Thr	
	230					235					240					
GTT	GTC	ATC	ATC	CTG	GGG	GCG	TTC	GTG	GTC	TGC	TGG	ACA	CCA	GGC	CAG	1663
Val	Val	Ile	Ile	Leu	Gly	Ala	Phe	Val	Val	Cys	Trp	Thr	Pro	Gly	Gln	
245					250					255					260	
GTG	GTA	CTG	CTC	CTG	GAT	GGT	TTA	GGC	TGT	GAG	TCC	TGC	AAT	GTC	CTG	1711
Val	Val	Leu	Leu	Leu	Asp	Gly	Leu	Gly	Cys	Glu	Ser	Cys	Asn	Val	Leu	
				265					270					275		
GCG	TTA	GAA	AAG	TAC	TTC	CTA	CTG	TTG	GCC	GAG	CCA	ACC	TCA	CTG	GTC	1759
Ala	Leu	Glu	Lys	Tyr	Phe	Leu	Leu	Leu	Ala	Glu	Pro	Thr	Ser	Leu	Val	
			280					285					290			
AAT	GCT	GCT	GTG	TAC	TCT	TGC	CGA	GAT	GCT	GAG	ATG	CGC	CGC	ACC	TTC	1807
Asn	Ala	Ala	Val	Tyr	Ser	Cys	Arg	Asp	Ala	Glu	Met	Arg	Arg	Thr	Phe	
	295						300					305				
CGC	CGC	CTT	CTC	CTG	CTG	CGC	GTG	CCT	CCG	CCA	GTC	CAC	CCG	CGA	GTC	1855
Arg	Arg	Leu	Leu	Leu	Leu	Arg	Val	Pro	Pro	Pro	Val	His	Pro	Arg	Val	
	310					315					320					

TGT CCA CTA TAC ATC CTC TGC CCA GGG AGG TGC CAG CAC TCG CAT CAT	1903
Cys Pro Leu Tyr Ile Leu Cys Pro Gly Arg Cys Gln His Ser His His	
325 330 335 340	
GCT TCC CGA GAA CGG CCA CCC ACT GAT GGA CTC CAC CCT TTA GCT ACC	1951
Ala Ser Arg Glu Arg Pro Pro Thr Asp Gly Leu His Pro Leu Ala Thr	
345 350 355	
TTG AAC TAC AGC GGT ACG CGG CAA GCA ACA AAT CCA CAG CCC CTG ATG	1999
Leu Asn Tyr Ser Gly Thr Arg Gln Ala Thr Asn Pro Gln Pro Leu Met	
360 365 370	
ACT TGT GGG TGC TCC TGG CTC AAC CCA ACC TCG TGC CGA ATT CCT GCA	2047
Thr Cys Gly Cys Ser Trp Leu Asn Pro Thr Ser Cys Arg Ile Pro Ala	
375 380 385	
GCC CGG GGG ATC CAC TAG TTCTAGAGCG GCGCCACCGC GGTGGAGCTC	2095
Ala Arg Gly Ile His	
390	
CAGCTTTTGT TCCCTTTAGT GAGGGTTAAT TTCGAGCTTG GCGTAATCAT GGTCATAGCT	2155
GTTTCCTGTG TGAAATTGTT ATCCGCTCAC	2185

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Pro Thr Trp Ala Gly Trp Leu Met Arg Trp Cys Cys Pro Pro	
1 5 10 15	
Ala Asp Thr Arg Cys Thr Thr Phe Leu Cys Ser Gly Arg Ala Ala Pro	
20 25 30	
Gln Gln Ala Gly Ala Pro Gly His His Pro Lys Tyr Ser Leu Phe Pro	
35 40 45	
Trp Ile Trp Lys Val Arg Gly Leu Leu Pro Pro Pro Leu Thr Thr Asp	
50 55 60	
Val Val Pro Val Arg Leu Thr Leu Arg Ala Asn Leu Ser Ala Ala Asp	
65 70 75 80	
Leu Leu Arg Gly Arg Gly Leu Pro Leu Pro His Val Pro His Cys Pro	
85 90 95	
Arg Thr Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu	
100 105 110	
Leu Asp Thr Asn Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala	
115 120 125	
Val Glu Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu	
130 135 140	

Pro	Arg	Gly	Arg	Val	Val	Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	145	150	155	160
Leu	Gly	Leu	Gly	Leu	Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala	165	170	175	
Leu	Asp	Arg	Ser	Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu	180	185	190	
Ala	Val	Trp	Ala	Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala	195	200	205	
Val	Tyr	Thr	Arg	Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met	210	215	220	
Ala	Glu	His	Val	Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser	225	230	235	240
Leu	Val	Lys	Thr	Val	Val	Ile	Ile	Leu	Gly	Ala	Phe	Val	Val	Cys	Trp	245	250	255	
Thr	Pro	Gly	Gln	Val	Val	Leu	Leu	Leu	Asp	Gly	Leu	Gly	Cys	Glu	Ser	260	265	270	
Cys	Asn	Val	Leu	Ala	Leu	Glu	Lys	Tyr	Phe	Leu	Leu	Leu	Ala	Glu	Pro	275	280	285	
Thr	Ser	Leu	Val	Asn	Ala	Ala	Val	Tyr	Ser	Cys	Arg	Asp	Ala	Glu	Met	290	295	300	
Arg	Arg	Thr	Phe	Arg	Arg	Leu	Leu	Leu	Leu	Arg	Val	Pro	Pro	Pro	Val	305	310	315	320
His	Pro	Arg	Val	Cys	Pro	Leu	Tyr	Ile	Leu	Cys	Pro	Gly	Arg	Cys	Gln	325	330	335	
His	Ser	His	His	Ala	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Asp	Gly	Leu	His	340	345	350	
Pro	Leu	Ala	Thr	Leu	Asn	Tyr	Ser	Gly	Thr	Arg	Gln	Ala	Thr	Asn	Pro	355	360	365	
Gln	Pro	Leu	Met	Thr	Cys	Gly	Cys	Ser	Trp	Leu	Asn	Pro	Thr	Ser	Cys	370	375	380	
Arg	Ile	Pro	Ala	Ala	Arg	Gly	Ile	His								385	390		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 62..940



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCACGAGC ATAAGAAGAC AGAGAGAACT GAGTATCCTC CCAAAGGTGA CACTGGAAGC	60
A ATG AAC ACC ACA GTA ATG CAA GGC TTC AAC AGA TCT AAG CGG TGC	106
Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Lys Arg Cys	
1 5 10 15	
CCC AAA GAC ACT CGG ATA GTA CAG CTG GTA TTC CCA GCC CTC TAC ACA	154
Pro Lys Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr	
20 25 30	
GTG GTT TTC TTG ACC GGA ATC CTG CTG AAT ACT TTG GCT CTG TGG GTG	202
Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val	
35 40 45	
TTT GTT CAC ATC CCC AGC TCC TCC ACC TTC ATC ATC TAC CTC AAA AAC	250
Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn	
50 55 60	
ACT TTG GTG GCC GAC TTG ATA ATG ACA CTC ATG CTT CCT TTC AAA ATC	298
Thr Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile	
65 70 75	
CTC TCT GAC TCA CAC CTG GCA CCC TGG CAG CTC AGA GCT TTT GTG TGT	346
Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys	
80 85 90 95	
CGT TTT TCT TCG GTG ATA TTT TAT GAG ACC ATG TAT GTG GGC ATC GTG	394
Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val	
100 105 110	
CTG TTA GGG CTC ATA GCC TTT GAC AGA TTC CTC AAG ATC ATC AGA CCT	442
Leu Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro	
115 120 125	
TTG AGA AAT ATT TTT CTA AAA AAA CCT GTT TGG GGA AAA ACG GTC TCA	490
Leu Arg Asn Ile Phe Leu Lys Lys Pro Val Trp Gly Lys Thr Val Ser	
130 135 140	
ATC TTC ATC TGG TTC TTT TGG TTC TTC ATC TCC CTG CCA AAT ATG ATC	538
Ile Phe Ile Trp Phe Phe Trp Phe Phe Ile Ser Leu Pro Asn Met Ile	
145 150 155	
TTG AGC AAC AAG GAA GCA ACA CCA TCG TCT GTG AAA AAG TGT GCT TCC	586
Leu Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser	
160 165 170 175	
TTA AAG GGG CCT CTG GGG CTG AAA TGG CAT CAA ATG GTA AAT AAC ATA	634
Leu Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile	
180 185 190	
TGC CAG TTT ATT TTC TGG ACT GTT TTT ATC CTA ATG CTT GTG TTT TAT	682
Cys Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr	
195 200 205	
GTG GTT ATT GCA AAA AAG TAT ATG ATT CTT ATA GAA AGT CCA AAA GTA	730
Val Val Ile Ala Lys Lys Tyr Met Ile Leu Ile Glu Ser Pro Lys Val	
210 215 220	
AGG ACA GAA AAA ACA ACA AAA AGC TGG AAG GCA AAG TAT TTG TTG TCG	778

Arg	Thr	Glu	Lys	Thr	Thr	Lys	Ser	Trp	Lys	Ala	Lys	Tyr	Leu	Leu	Ser		
225						230					235						
TGG	CTG	TCT	TCT	TTG	TGT	GTT	TTG	CTC	CAT	TTC	ATT	TCG	CCA	GAG	TTC	826	
Trp	Leu	Ser	Ser	Leu	Cys	Val	Leu	Leu	His	Phe	Ile	Ser	Pro	Glu	Phe		
240					245					250					255		
CAT	ATA	CTC	ACA	GTC	AAA	CCA	ACA	ATA	AGA	CTG	ACT	GTA	GAC	TGC	AAA	874	
His	Ile	Leu	Thr	Val	Lys	Pro	Thr	Ile	Arg	Leu	Thr	Val	Asp	Cys	Lys		
				260					265					270			
ATC	AAC	TGT	TTA	TTG	CTA	AAG	AAA	CAA	CTC	TCT	TTT	TGG	CAG	CAA	CTA	922	
Ile	Asn	Cys	Leu	Leu	Leu	Lys	Lys	Gln	Leu	Ser	Phe	Trp	Gln	Gln	Leu		
			275					280					285				
ACA	TTT	GTA	TGG	ATC	CCT	TAA	TATACATATT	CTTATGTAAA	AAATTCACAG							973	
Thr	Phe	Val	Trp	Ile	Pro												
		290															
AAAAGCTACC	ATGTATGCAA	GGGAGAAAGA	CCACAGCATC	AAGCCAAGAA	AATCATAGCA											1033	
GTCAGACAGA	CAACATAACC	TTAGGCTGAC	AACTGTACAT	AGGGGTAAC	TCTATTTATT											1093	
GATGAGACTT	CCGTAGATAA	TGTGGAAATC	CAATTTAACC	AAGAAAAAAA	GATTGGGGCA											1153	
AATGCTCTCT	TACATTTTAT	TATCCTGGTG	TACAGAAAAG	ATTATATAAA	ATTTAAATCC											1213	
ACATAGATCT	ATTCATAAGC	TGAATGAACC	ATTACTAAGA	GAATGCAACA	GGATACAAAT											1273	
GGCCACTAGA	GGTCATTATT	TCTTTCTTTC	TTTCTTTTTT	TTTTTTTAAT	TTCAAGAGCA											1333	
TTTCACTTTA	ACATTTTGGA	AAAGACTAAG	GAGAAACGTA	TATCCCTACA	AACCTCCCCT											1393	
CCAAACACCT	TCTTACATTC	TTTTCCACAA	TTACATAAC	ACTACTGCTT	TTGTGCCCCCT											1453	
TAAATGTAGA	TTTGTTGGCT	G														1474	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Lys	Arg	Cys	Pro
1				5					10					15	
Lys	Asp	Thr	Arg	Ile	Val	Gln	Leu	Val	Phe	Pro	Ala	Leu	Tyr	Thr	Val
			20					25					30		
Val	Phe	Leu	Thr	Gly	Ile	Leu	Leu	Asn	Thr	Leu	Ala	Leu	Trp	Val	Phe
		35					40					45			
Val	His	Ile	Pro	Ser	Ser	Ser	Thr	Phe	Ile	Ile	Tyr	Leu	Lys	Asn	Thr
	50					55					60				
Leu	Val	Ala	Asp	Leu	Ile	Met	Thr	Leu	Met	Leu	Pro	Phe	Lys	Ile	Leu

65		70		75		80									
Ser	Asp	Ser	His	Leu	Ala	Pro	Trp	Gln	Leu	Arg	Ala	Phe	Val	Cys	Arg
				85					90					95	
Phe	Ser	Ser	Val	Ile	Phe	Tyr	Glu	Thr	Met	Tyr	Val	Gly	Ile	Val	Leu
			100					105					110		
Leu	Gly	Leu	Ile	Ala	Phe	Asp	Arg	Phe	Leu	Lys	Ile	Ile	Arg	Pro	Leu
		115					120					125			
Arg	Asn	Ile	Phe	Leu	Lys	Lys	Pro	Val	Trp	Gly	Lys	Thr	Val	Ser	Ile
	130						135					140			
Phe	Ile	Trp	Phe	Phe	Trp	Phe	Phe	Ile	Ser	Leu	Pro	Asn	Met	Ile	Leu
145					150					155					160
Ser	Asn	Lys	Glu	Ala	Thr	Pro	Ser	Ser	Val	Lys	Lys	Cys	Ala	Ser	Leu
				165					170					175	
Lys	Gly	Pro	Leu	Gly	Leu	Lys	Trp	His	Gln	Met	Val	Asn	Asn	Ile	Cys
			180					185					190		
Gln	Phe	Ile	Phe	Trp	Thr	Val	Phe	Ile	Leu	Met	Leu	Val	Phe	Tyr	Val
		195					200					205			
Val	Ile	Ala	Lys	Lys	Tyr	Met	Ile	Leu	Ile	Glu	Ser	Pro	Lys	Val	Arg
	210					215					220				
Thr	Glu	Lys	Thr	Thr	Lys	Ser	Trp	Lys	Ala	Lys	Tyr	Leu	Leu	Ser	Trp
225					230					235					240
Leu	Ser	Ser	Leu	Cys	Val	Leu	Leu	His	Phe	Ile	Ser	Pro	Glu	Phe	His
				245					250					255	
Ile	Leu	Thr	Val	Lys	Pro	Thr	Ile	Arg	Leu	Thr	Val	Asp	Cys	Lys	Ile
			260					265					270		
Asn	Cys	Leu	Leu	Leu	Lys	Lys	Gln	Leu	Ser	Phe	Trp	Gln	Gln	Leu	Thr
		275					280					285			
Phe	Val	Trp	Ile	Pro											
	290														

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 161..1192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTGGGTAT TTCTGAGAAA AAGGAAATAT TTATAAAACC ATCCAAAGAT CCAGATAATT	60
TGCAAATAAA TTGGAGGTTA TAGAGGTTAT AATCTGAATC CCAAAGGAGA CTGCAGCTGA	120
TGAAAGTGCT TCCAAACTGA AAATTGGACG TGCCTTTACG ATG GTA AGC GTT AAC Met Val Ser Val Asn 1 5	175
AGC TCC CAC TGC TTC TAT AAT GAC TCC TTT AAG TAC ACT TTG TAT GGG Ser Ser His Cys Phe Tyr Asn Asp Ser Phe Lys Tyr Thr Leu Tyr Gly 10 15 20	223
TGC ATG TTC AGC ATG GTG TTT GTG CTT GGG TTA ATA TCC AAT TGT GTT Cys Met Phe Ser Met Val Phe Val Leu Gly Leu Ile Ser Asn Cys Val 25 30 35	271
GCC ATA TAC ATT TTC ATC TGC GTC CTC AAA GTC CGA AAT GAA ACT ACA Ala Ile Tyr Ile Phe Ile Cys Val Leu Lys Val Arg Asn Glu Thr Thr 40 45 50	319
ACT TAC ATG ATT AAC TTG GCA ATG TCA GAC TTG CTT TTT GTT TTT ACT Thr Tyr Met Ile Asn Leu Ala Met Ser Asp Leu Leu Phe Val Phe Thr 55 60 65	367
TTA CCC TTC AGG ATT TTT TAC TTC ACA ACA CGG AAT TGG CCA TTT GGA Leu Pro Phe Arg Ile Phe Tyr Phe Thr Thr Arg Asn Trp Pro Phe Gly 70 75 80 85	415
GAT TTA CTT TGT AAG ATT TCT GTG ATG CTG TTT TAT ACC AAC ATG TAC Asp Leu Leu Cys Lys Ile Ser Val Met Leu Phe Tyr Thr Asn Met Tyr 90 95 100	463
GGA AGC ATT CTG TTC TTA ACC TGT ATT AGT GTA GAT CGA TTT CTG GCA Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala 105 110 115	511
ATT GTC TAC CCA TTT AAG TCA AAG ACT CTA AGA ACC AAA AGA AAT GCA Ile Val Tyr Pro Phe Lys Ser Lys Thr Leu Arg Thr Lys Arg Asn Ala 120 125 130	559
AAG ATT GTT TGC ACT GGC GTG TGG TTA ACT GTG ATC GGA GGA AGT GCA Lys Ile Val Cys Thr Gly Val Trp Leu Thr Val Ile Gly Gly Ser Ala 135 140 145	607
CCC GCC GTT TTT GTT CAG TCT ACC CAC TCT CAG GGT AAC AAT GCC TCA Pro Ala Val Phe Val Gln Ser Thr His Ser Gln Gly Asn Asn Ala Ser 150 155 160 165	655
GAA GCC TGC TTT GAA AAT TTT CCA GAA GCC ACA TGG AAA ACA TAT CTC Glu Ala Cys Phe Glu Asn Phe Pro Glu Ala Thr Trp Lys Thr Tyr Leu 170 175 180	703
TCA AGG ATT GTA ATT TTC ATC GAA ATA GTG GGA TTT TTT ATT CCT CTA Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly Phe Phe Ile Pro Leu 185 190 195	751
ATT TTA AAT GTA ACT TGT TCT AGT ATG GTG CTA AAA ACT TTA ACC AAA Ile Leu Asn Val Thr Cys Ser Ser Met Val Leu Lys Thr Leu Thr Lys 200 205 210	799
CCT GTT ACA TTA AGT AGA AGC AAA ATA AAC AAA ACT AAG GTT TTA AAA Pro Val Thr Leu Ser Arg Ser Lys Ile Asn Lys Thr Lys Val Leu Lys	847

215	220	225	
ATG ATT TTT GTA CAT TTG ATC ATA TTC TGT TTC TGT TTT GTT CCT TAC			895
Met Ile Phe Val His Leu Ile Ile Phe Cys Phe Cys Phe Val Pro Tyr			
230	235	240	245
AAT ATC AAT CTT ATT TTA TAT TCT CTT GTG AGA ACA CAA ACA TTT GTT			943
Asn Ile Asn Leu Ile Leu Tyr Ser Leu Val Arg Thr Gln Thr Phe Val			
	250	255	260
AAT TGC TCA GTA GTG GCA GCA GTA AGG ACA ATG TAC CCA ATC ACT CTC			991
Asn Cys Ser Val Val Ala Ala Val Arg Thr Met Tyr Pro Ile Thr Leu			
	265	270	275
TGT ATT GCT GTT TCC AAC TGT TGT TTT GAC CCT ATA GTT TAC TAC TTT			1039
Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro Ile Val Tyr Tyr Phe			
	280	285	290
ACA TCG GAC ACA ATT CAG AAT TCA ATA AAA ATG AAA AAC TGG TCT GTC			1087
Thr Ser Asp Thr Ile Gln Asn Ser Ile Lys Met Lys Asn Trp Ser Val			
	295	300	305
AGG AGA AGT GAC TTC AGA TTC TCT GAA GTT CAT GGT GCA GAG AAT TTT			1135
Arg Arg Ser Asp Phe Arg Phe Ser Glu Val His Gly Ala Glu Asn Phe			
	310	315	320
ATT CAG CAT AAC CTA CAG ACC TTA AAA AGT AAG ATA TTT GAC AAT GAA			1183
Ile Gln His Asn Leu Gln Thr Leu Lys Ser Lys Ile Phe Asp Asn Glu			
	330	335	340
TCT GCT GCC TGA AATAAAACCA TTAGGACTCA CTGGGACAGA ACTTTCAAGT			1235
Ser Ala Ala			
TCCTTCAACT GTGAAAAGTG TCTTTTTGGA CAAACTATTT TTCCACCTCC AAAAGAAATT			1295
AACACA			1301

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Val	Ser	Val	Asn	Ser	Ser	His	Cys	Phe	Tyr	Asn	Asp	Ser	Phe	Lys
1				5					10					15	
Tyr	Thr	Leu	Tyr	Gly	Cys	Met	Phe	Ser	Met	Val	Phe	Val	Leu	Gly	Leu
			20					25					30		
Ile	Ser	Asn	Cys	Val	Ala	Ile	Tyr	Ile	Phe	Ile	Cys	Val	Leu	Lys	Val
		35					40					45			
Arg	Asn	Glu	Thr	Thr	Thr	Tyr	Met	Ile	Asn	Leu	Ala	Met	Ser	Asp	Leu
	50					55					60				

Leu	Phe	Val	Phe	Thr	Leu	Pro	Phe	Arg	Ile	Phe	Tyr	Phe	Thr	Thr	Arg
65					70					75					80
Asn	Trp	Pro	Phe	Gly	Asp	Leu	Leu	Cys	Lys	Ile	Ser	Val	Met	Leu	Phe
			85						90					95	
Tyr	Thr	Asn	Met	Tyr	Gly	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val
		100						105					110		
Asp	Arg	Phe	Leu	Ala	Ile	Val	Tyr	Pro	Phe	Lys	Ser	Lys	Thr	Leu	Arg
		115					120					125			
Thr	Lys	Arg	Asn	Ala	Lys	Ile	Val	Cys	Thr	Gly	Val	Trp	Leu	Thr	Val
	130					135					140				
Ile	Gly	Gly	Ser	Ala	Pro	Ala	Val	Phe	Val	Gln	Ser	Thr	His	Ser	Gln
145					150					155					160
Gly	Asn	Asn	Ala	Ser	Glu	Ala	Cys	Phe	Glu	Asn	Phe	Pro	Glu	Ala	Thr
			165						170					175	
Trp	Lys	Thr	Tyr	Leu	Ser	Arg	Ile	Val	Ile	Phe	Ile	Glu	Ile	Val	Gly
			180					185					190		
Phe	Phe	Ile	Pro	Leu	Ile	Leu	Asn	Val	Thr	Cys	Ser	Ser	Met	Val	Leu
		195					200					205			
Lys	Thr	Leu	Thr	Lys	Pro	Val	Thr	Leu	Ser	Arg	Ser	Lys	Ile	Asn	Lys
	210					215					220				
Thr	Lys	Val	Leu	Lys	Met	Ile	Phe	Val	His	Leu	Ile	Ile	Phe	Cys	Phe
225					230					235					240
Cys	Phe	Val	Pro	Tyr	Asn	Ile	Asn	Leu	Ile	Leu	Tyr	Ser	Leu	Val	Arg
				245					250					255	
Thr	Gln	Thr	Phe	Val	Asn	Cys	Ser	Val	Val	Ala	Ala	Val	Arg	Thr	Met
			260					265					270		
Tyr	Pro	Ile	Thr	Leu	Cys	Ile	Ala	Val	Ser	Asn	Cys	Cys	Phe	Asp	Pro
		275					280					285			
Ile	Val	Tyr	Tyr	Phe	Thr	Ser	Asp	Thr	Ile	Gln	Asn	Ser	Ile	Lys	Met
	290					295					300				
Lys	Asn	Trp	Ser	Val	Arg	Arg	Ser	Asp	Phe	Arg	Phe	Ser	Glu	Val	His
305					310					315					320
Gly	Ala	Glu	Asn	Phe	Ile	Gln	His	Asn	Leu	Gln	Thr	Leu	Lys	Ser	Lys
				325					330					335	
Ile	Phe	Asp	Asn	Glu	Ser	Ala	Ala								
			340												

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
GACTAAAGCT TAATGAGTAG TGAAATGGTG 30
- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 31 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:  
GAACTTCTAG ACCCTCAGGG TTGTAAATCA G 31
- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
GACTAAAGCT TAATGAGGCC CACATGGGCA 30
- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 32 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
GAACTTCTAG ACGAACTAGT GGATCCCCC GG 32
- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
GACTAAAGCT TAATGGCGTC TTTCTCTGCT 30
- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS
    - (A) LENGTH: 30 BASE PAIRS
    - (B) TYPE: NUCLEIC ACID
    - (C) STRANDEDNESS: SINGLE
    - (D) TOPOLOGY: LINEAR
  - (ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
GAACTTCTAG ACTTCACACA GTTGTACTAT 30

- (2) INFORMATION FOR SEQ ID NO:15:  
(i) SEQUENCE CHARACTERISTICS  
    (A) LENGTH: 30 BASE PAIRS  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
GACTAAAGCT TAATGGTAAG CGTTAACAGC 30

- (2) INFORMATION FOR SEQ ID NO:16:  
(i) SEQUENCE CHARACTERISTICS  
    (A) LENGTH: 31 BASE PAIRS  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
GAACTTCTAG ACTTCAGGCA GCAGATTCAT T 31

- (2) INFORMATION FOR SEQ ID NO:17:  
(i) SEQUENCE CHARACTERISTICS  
    (A) LENGTH: 34 BASE PAIRS  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
GTCCAAGCTT GCCACCATGA GTAGTGAAAT GGTG 34

- (2) INFORMATION FOR SEQ ID NO:18:  
(i) SEQUENCE CHARACTERISTICS  
    (A) LENGTH: 58 BASE PAIRS  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGGTTGT AAATCAGG 58

- (2) INFORMATION FOR SEQ ID NO:19:  
(i) SEQUENCE CHARACTERISTICS  
    (A) LENGTH: 34 BASE PAIRS  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: SINGLE  
    (D) TOPOLOGY: LINEAR  
  
(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
GTCCAAGCTT GCCACCATGG TTGGTGGCAC CTGG 34



(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 58 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGTGGATC CCCC GTGC 58

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 34 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
GTCCAAGCTT GCCACCATGA ACACCACAGT AATG 34

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 61 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAAGGGATC CATACAAATG 60  
T 61

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 34 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
GTCCAAGCTT GCCACCATGG TAAGCGTTAA CAGC 34

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 61 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:  
CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGCAGCA GATTCATTGT 60  
C 61

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 30 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:  
CGGGATCCCT CCATGAGTAG TGAAATGGTG 30

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 29 BASE PAIRS
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:  
CGGGATCCCG CTCAGGGTTG TAAATCAGG 29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 222 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Phe	Phe	Leu	Ser	His	Leu	Ala	Ile	Val	Asp	Ile	Ala	Tyr	Ala	Cys	Asn	
1				5					10					15		
Thr	Val	Pro	Gln	Met	Leu	Val	Asn	Leu	Leu	Asp	Pro	Val	Lys	Pro	Ile	
			20					25					30			
Ser	Tyr	Ala	Gly	Cys	Met	Thr	Gln	Thr	Phe	Leu	Phe	Leu	Thr	Phe	Ala	
		35					40					45				
Ile	Thr	Glu	Cys	Leu	Leu	Leu	Val	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Val	
	50					55					60					
Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr	Ser	Ala	Ile	Met	Ser	Trp	Arg	Val	
65					70					75					80	
Cys	Ser	Thr	Met	Ala	Val	Thr	Ser	Trp	Ile	Ile	Gly	Val	Leu	Leu	Ser	
			85						90					95		
Leu	Ile	His	Leu	Val	Leu	Leu	Leu	Pro	Leu	Pro	Phe	Cys	Val	Ser	Gln	
			100					105					110			

Lys Val Asn His Phe Phe Cys Glu Ile Thr Ala Ile Leu Lys Leu Ala  
115 120 125  
Cys Ala Asp Thr His Leu Asn Glu Thr Met Val Leu Ala Gly Ala Val  
130 135 140  
Ser Val Leu Val Gly Pro Phe Ser Ser Ile Val Val Ser Tyr Ala Cys  
145 150 155 160  
Ile Leu Gly Ala Ile Leu Lys Ile Gln Ser Glu Glu Gly Gln Arg Lys  
165 170 175  
Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Gly Leu Phe Tyr  
180 185 190  
Gly Thr Ala Ile Val Met Tyr Val Gly Pro Arg His Gly Ser Pro Lys  
195 200 205  
Glu Gln Lys Lys Tyr Leu Leu Leu Phe His Ser Leu Phe Asn  
210 215 220

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val  
1 5 10 15  
Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr  
20 25 30  
Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr  
35 40 45  
Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile  
50 55 60  
Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met  
65 70 75 80  
Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val  
85 90 95  
Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu  
100 105 110  
Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu  
115 120 125  
Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile  
130 135 140

Thr	Met	Leu	Lys	Met	Lys	Leu	His	Asn	Gly	Ser	Asn	Asn	Phe	Arg	Leu	145	150	155	160
Phe	Leu	Leu	Ile	Ser	Ala	Cys	Trp	Val	Ile	Ser	Leu	Ile	Leu	Gly	Gly	165	170	175	
Leu	Pro	Ile	Met	Gly	Trp	Asn	Cys	Ile	Ser	Ala	Leu	Ser	Ser	Cys	Ser	180	185	190	
Thr	Val	Leu	Pro	Leu	Tyr	His	Lys	His	Tyr	Ile	Leu	Phe	Cys	Thr	Thr	195	200	205	
Val	Phe	Thr	Leu	Leu	Leu	Leu	Ser	Ile	Val	Ile	Leu	Tyr	Cys	Arg	Ile	210	215	220	
Tyr	Ser	Leu	Val	Arg	Thr	Arg	Ser	Arg	Arg	Leu	Thr	Phe	Arg	Lys	Asn	225	230	235	240
Ile	Ser	Lys	Ala	Ser	Arg	Ser	Ser	Glu	Asn	Val	Ala	Leu	Leu	Lys	Thr	245	250	255	
Val	Ile	Ile	Val	Leu	Ser	Val	Phe	Ile	Ala	Cys	Trp	Ala	Pro	Leu	Phe	260	265	270	
Ile	Leu	Leu	Leu	Leu	Asp	Val	Gly	Cys	Lys	Val	Lys	Thr	Cys	Asp	Ile	275	280	285	
Leu	Phe	Arg	Ala	Glu	Tyr	Phe	Leu	Val	Leu	Ala	Val	Leu	Asn	Ser	Gly	290	295	300	
Thr	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Thr	Asn	Lys	Glu	Met	Arg	Arg	Ala	305	310	315	320
Phe	Ile	Arg	Ile	Met	Ser	Cys	Cys	Lys	Cys	Pro	Ser	Gly	Asp	Ser	Ala	325	330	335	
Gly	Lys	Phe	Lys	Arg	Pro	Ile	Ile	Ala	Gly	Met	Glu	Phe	Ser	Arg	Ser	340	345	350	
Lys	Ser	Asp	Asn	Ser	Ser	His	Pro	Gln	Lys	Asp	Glu	Gly	Asp	Asn	Pro	355	360	365	
Glu	Thr	Ile	Met	Ser	Ser	Gly	Asn	Val	Asn	Ser	Ser	Ser				370	375	380	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ile	Asn	Ser	Thr	Ser	Thr	Gln	Pro	Pro	Asp	Glu	Ser	Cys	Ser	Gln	Asn
1				5					10					15	

Leu	Leu	Ile	Thr	Gln	Gln	Ile	Ile	Pro	Val	Leu	Tyr	Cys	Met	Val	Phe	20	25	30
Ile	Ala	Gly	Ile	Leu	Leu	Asn	Gly	Val	Ser	Gly	Trp	Ile	Phe	Phe	Tyr	35	40	45
Val	Pro	Ser	Ser	Lys	Ser	Phe	Ile	Ile	Tyr	Leu	Lys	Asn	Ile	Val	Ile	50	55	60
Ala	Asp	Phe	Val	Met	Ser	Leu	Thr	Phe	Pro	Phe	Lys	Ile	Leu	Gly	Asp	65	70	75
Ser	Gly	Leu	Gly	Pro	Trp	Gln	Leu	Asn	Val	Phe	Val	Cys	Arg	Val	Ser	85	90	95
Ala	Val	Leu	Phe	Tyr	Val	Asn	Met	Tyr	Val	Ser	Ile	Val	Phe	Phe	Gly	100	105	110
Leu	Ile	Ser	Phe	Asp	Arg	Tyr	Tyr	Lys	Ile	Val	Lys	Pro	Leu	Trp	Thr	115	120	125
Ser	Phe	Ile	Gln	Ser	Val	Ser	Tyr	Ser	Lys	Leu	Leu	Ser	Val	Ile	Val	130	135	140
Trp	Met	Leu	Met	Leu	Leu	Leu	Ala	Val	Pro	Asn	Ile	Ile	Leu	Thr	Asn	145	150	155
Gln	Ser	Val	Arg	Glu	Val	Thr	Gln	Ile	Lys	Cys	Ile	Glu	Leu	Lys	Ser	165	170	175
Glu	Leu	Gly	Arg	Lys	Trp	His	Lys	Ala	Ser	Asn	Tyr	Ile	Phe	Val	Ala	180	185	190
Ile	Phe	Trp	Ile	Val	Phe	Leu	Leu	Leu	Ile	Val	Phe	Tyr	Thr	Ala	Ile	195	200	205
Thr	Lys	Lys	Ile	Phe	Lys	Ser	His	Leu	Lys	Ser	Ser	Arg	Asn	Ser	Thr	210	215	220
Ser	Val	Lys	Lys	Lys	Ser	Ser	Arg	Asn	Ile	Phe	Ser	Ile	Val	Phe	Val	225	230	235
Phe	Phe	Val	Cys	Phe	Val	Pro	Tyr	His	Ile	Ala	Arg	Ile	Pro	Tyr	Thr	245	250	255
Lys	Ser	Gln	Thr	Glu	Ala	His	Tyr	Ser	Cys	Gln	Ser	Lys	Glu	Ile	Leu	260	265	270
Arg	Tyr	Met	Lys	Glu	Phe	Thr	Leu	Leu	Leu	Ser	Ala	Ala	Asn	Val	Cys	275	280	285
Leu	Asp	Pro	Ile	Ile	Tyr	Phe	Phe	Leu	Cys	Gln	Pro	Phe	Arg	Glu	Ile	290	295	300
Leu	Cys	Lys	Lys	Leu	His	Ile	Pro	Leu	Lys	Ala	Gln	Asn	Asp	Leu	Asp	305	310	315
Ile	Ser	Arg	Ile	Lys												325		

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 302 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser	Ser	Asn	Cys	Ser	Thr	Glu	Asp	Ser	Phe	Lys	Tyr	Thr	Leu	Tyr	Gly	1	5	10	15
Cys	Val	Phe	Ser	Met	Val	Phe	Val	Leu	Gly	Leu	Ile	Ala	Asn	Cys	Val	20	25	30	
Ala	Ile	Tyr	Ile	Phe	Thr	Phe	Thr	Leu	Lys	Val	Arg	Asn	Glu	Thr	Thr	35	40	45	
Thr	Tyr	Met	Leu	Met	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Val	Phe	Thr	50	55	60	
Leu	Pro	Phe	Arg	Ile	Tyr	Tyr	Phe	Val	Val	Arg	Asn	Trp	Pro	Phe	Gly	65	70	75	80
Asp	Val	Leu	Cys	Lys	Ile	Ser	Val	Thr	Leu	Phe	Tyr	Thr	Asn	Met	Tyr	85	90	95	
Gly	Ser	Ile	Leu	Phe	Leu	Thr	Cys	Ile	Ser	Val	Asp	Arg	Phe	Leu	Ala	100	105	110	
Ile	Val	His	Pro	Phe	Arg	Ser	Lys	Thr	Leu	Arg	Thr	Lys	Arg	Asn	Ala	115	120	125	
Arg	Ile	Val	Cys	Val	Ala	Val	Trp	Ile	Thr	Val	Leu	Ala	Gly	Ser	Thr	130	135	140	
Pro	Ala	Ser	Phe	Phe	Gln	Ser	Thr	Asn	Arg	Gln	Asn	Asn	Thr	Glu	Gln	145	150	155	160
Arg	Thr	Cys	Phe	Glu	Asn	Phe	Pro	Glu	Ser	Thr	Trp	Lys	Thr	Tyr	Leu	165	170	175	
Ser	Arg	Ile	Val	Ile	Phe	Ile	Glu	Ile	Val	Gly	Phe	Phe	Ile	Pro	Leu	180	185	190	
Ile	Leu	Asn	Val	Thr	Cys	Ser	Thr	Met	Val	Leu	Arg	Thr	Leu	Asn	Lys	195	200	205	
Pro	Leu	Thr	Leu	Ser	Arg	Asn	Lys	Leu	Ser	Lys	Lys	Lys	Val	Leu	Lys	210	215	220	
Met	Ile	Phe	Val	His	Leu	Val	Ile	Phe	Cys	Phe	Cys	Phe	Val	Pro	Tyr	225	230	235	240
Asn	Ile	Thr	Leu	Ile	Leu	Tyr	Ser	Leu	Met	Arg	Thr	Gln	Thr	Trp	Ile	245	250	255	
Asn	Cys	Ser	Val	Val	Thr	Ala	Val	Arg	Thr	Met	Tyr	Pro	Val	Thr	Leu				

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			260					265				270			
Cys	Ile	Ala	Val	Ser	Asn	Cys	Cys	Phe	Asp	Pro	Ile	Val	Tyr	Tyr	Phe
		275					280					285			
Thr	Ser	Asp	Thr	Asn	Ser	Glu	Leu	Asp	Lys	Lys	Gln	Gln	Val		
	290					295					300				